



6

SEQUENCE LISTING

<110> PELLETIER, JERRY
GROS, PHILIPPE
DUBOW, MICHAEL

A¹

<120> COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
STAAU_R9

<130> 073406-0701

<140> 10/025,222

<141> 2001-12-19

<150> 60/256,349

<151> 2000-12-19

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1800

<212> DNA

<213> Staphylococcus aureus

<400> 1

ttgcgaatag	atcaatcgat	cattaatgaa	ataaaagata	aaaccgacat	tttagacttg	60
gtaagtgaat	atgtaaaatt	agaaaagaga	ggacgcaatt	atatagggtt	gtgtcctttt	120
catgatgaaa	agacaccttc	atttacagtt	tctgaagata	aacaaatttg	tcattgtttt	180
ggttgtaaaa	aaggtggcaa	tgtttttcaa	tttactcaag	aaattaaaga	catatcattt	240
gttgaagcgg	ttaaagaatt	aggtgataga	gttaatgttg	ctgtagatat	tgaggcaaca	300
caatctaact	caaattgttca	aattgcttct	gatgatttac	aaatgattga	aatgcatgag	360
ttaatacaag	aattttatta	ttacgcttta	acaaagacag	tcgaaggcga	acaagcatta	420
acgtacttac	aagaacgtgg	ttttacagat	gcgcttatta	aagagcgagg	cattggcttt	480
gcacccgata	gtcacattt	ttgtcatgat	tttcttcaaa	aaaaggggta	cgatattgaa	540
tttagcatatg	aagccggatt	attatcacgt	aacgaagaaa	atttcagtta	ttacgataga	600
tttcgaaatc	gtattatggt	tcctttgaaa	aatgcgcaag	gaagaattgt	tggatattca	660
ggtcgaacat	ataccgggtca	agaaccaaaa	tacttaaata	gtcctgaaac	acctatcttt	720
caaaaaagaa	agttgttata	caacttagat	aaagcgcgta	aatcaattag	aaaattagat	780
gaaatcgtat	tactagaagg	ttttatggat	gttataaaat	ctgatactgc	tggcttgaaa	840
aacgttggtg	caacaatggg	tacacagttg	tcagatgaac	atattacttt	tatacgaaag	900
ttaacatcaa	atataacatt	aatgtttgat	ggggattttg	cgggtagtga	agcaacactt	960
aaaacaggtc	aaaatttggt	acagcaaggg	ctaaatgtat	ttgttataca	attgccatca	1020
ggcatggatc	cggatgaata	cattggtaag	tatggcaacg	atgcatttac	tgcttttgta	1080
aaaaatgaca	aaaagtcatt	tgcacattat	aaagtgaagta	tattaaaga	tgaaattgca	1140
cataatgacc	tttcatatga	acgttatattg	aaagaactaa	gtcatgatat	ttcgcttatg	1200
aaatcatcga	ttttgcaaca	aaaggcttta	aatgatgttg	caccattttt	caatgttagt	1260
cctgagcaat	tagctaacga	aatacaattc	aatcaagcac	cagccaatta	ttatccagaa	1320
gatgagtatg	gcggttacat	tgaacctgag	ccaattggta	tggcacaatt	tgacaatttg	1380
agccgtcaag	aaaaagcgga	gcgagcattt	ttaaaacatt	taatgagaga	taaagataca	1440
tttttaaat	attatgaaa	tgttgataag	gataaacttca	caaatcagca	ttttaaatat	1500
gtattcgaag	tcttacatga	tttttatgcg	gaaaatgatc	aataataat	cagtgatgct	1560
gtgcagtatg	ttaattcaaa	tgagttgaga	gaaacactaa	ttagcttaga	acaatataat	1620
ttgaatgacg	aaccatagga	aatgaaatt	gatgattatg	tcaatgttat	taatgaaaaa	1680
ggacaagaaa	caattgagtc	attgaatcat	aaattaaggg	aagctacaag	gattggcgat	1740
gtagaattac	aaaaatacta	tttacagcaa	attgttgcta	agaataaaga	acgcatgtag	1800

STAPHYLOCOCCUS AUREUS

<210> 2
 <211> 599
 <212> PRT
 <213> Staphylococcus aureus

<400> 2

Leu	Arg	Ile	Asp	Gln	Ser	Ile	Ile	Asn	Glu	Ile	Lys	Asp	Lys	Thr	Asp	1	5	10	15
Ile	Leu	Asp	Leu	Val	Ser	Glu	Tyr	Val	Lys	Leu	Glu	Lys	Arg	Gly	Arg	20	25	30	
Asn	Tyr	Ile	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe	35	40	45	
Thr	Val	Ser	Glu	Asp	Lys	Gln	Ile	Cys	His	Cys	Phe	Gly	Cys	Lys	Lys	50	55	60	
Gly	Gly	Asn	Val	Phe	Gln	Phe	Thr	Gln	Glu	Ile	Lys	Asp	Ile	Ser	Phe	65	70	75	80
Val	Glu	Ala	Val	Lys	Glu	Leu	Gly	Asp	Arg	Val	Asn	Val	Ala	Val	Asp	85	90	95	
Ile	Glu	Ala	Thr	Gln	Ser	Asn	Ser	Asn	Val	Gln	Ile	Ala	Ser	Asp	Asp	100	105	110	
Leu	Gln	Met	Ile	Glu	Met	His	Glu	Leu	Ile	Gln	Glu	Phe	Tyr	Tyr	Tyr	115	120	125	
Ala	Leu	Thr	Lys	Thr	Val	Glu	Gly	Glu	Gln	Ala	Leu	Thr	Tyr	Leu	Gln	130	135	140	
Glu	Arg	Gly	Phe	Thr	Asp	Ala	Leu	Ile	Lys	Glu	Arg	Gly	Ile	Gly	Phe	145	150	155	160
Ala	Pro	Asp	Ser	Ser	His	Phe	Cys	His	Asp	Phe	Leu	Gln	Lys	Lys	Gly	165	170	175	
Tyr	Asp	Ile	Glu	Leu	Ala	Tyr	Glu	Ala	Gly	Leu	Leu	Ser	Arg	Asn	Glu	180	185	190	
Glu	Asn	Phe	Ser	Tyr	Tyr	Asp	Arg	Phe	Arg	Asn	Arg	Ile	Met	Phe	Pro	195	200	205	
Leu	Lys	Asn	Ala	Gln	Gly	Arg	Ile	Val	Gly	Tyr	Ser	Gly	Arg	Thr	Tyr	210	215	220	
Thr	Gly	Gln	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	Thr	Pro	Ile	Phe	225	230	235	240
Gln	Lys	Arg	Lys	Leu	Leu	Tyr	Asn	Leu	Asp	Lys	Ala	Arg	Lys	Ser	Ile	245	250	255	
Arg	Lys	Leu	Asp	Glu	Ile	Val	Leu	Leu	Glu	Gly	Phe	Met	Asp	Val	Ile	260	265	270	

Lys Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr
 275 280 285
 Gln Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn
 290 295 300
 Ile Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu
 305 310 315 320
 Lys Thr Gly Gln Asn Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile
 325 330 335
 Gln Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly
 340 345 350
 Asn Asp Ala Phe Thr Ala Phe Val Lys Asn Asp Lys Lys Ser Phe Ala
 355 360 365
 His Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu
 370 375 380
 Ser Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met
 385 390 395 400
 Lys Ser Ser Ile Leu Gln Gln Lys Ala Leu Asn Asp Val Ala Pro Phe
 405 410 415
 Phe Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln
 420 425 430
 Ala Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Ile Glu
 435 440 445
 Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn Leu Ser Arg Gln Glu
 450 455 460
 Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met Arg Asp Lys Asp Thr
 465 470 475 480
 Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp Asn Phe Thr Asn Gln
 485 490 495
 His Phe Lys Tyr Val Phe Glu Val Leu His Asp Phe Tyr Ala Glu Asn
 500 505 510
 Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr Val Asn Ser Asn Glu
 515 520 525
 Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr Asn Leu Asn Asp Glu
 530 535 540
 Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn Val Ile Asn Glu Lys
 545 550 555 560
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
 565 570 575

Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
 580 585 590

Ala Lys Asn Lys Glu Arg Met
 595

<210> 3
 <211> 216
 <212> DNA
 <213> Staphylococcus aureus

<400> 3
 atgaatataa tgcaattcaa aagcttattg aaatcgatgt atgaagagac aaagcaaagc 60
 gacccgattg tagcaaatgt atatatcgag actgggtggg cggatcaatag attgttggac 120
 aataacgagt tatcgctttt cgatgattac gacagagttg aaaagaaaat catgaatgaa 180
 atcaactgga agaaaacaca cattaaggag tgttaa 216

<210> 4
 <211> 71
 <212> PRT
 <213> Staphylococcus aureus

<400> 4
 Met Asn Ile Met Gln Phe Lys Ser Leu Leu Lys Ser Met Tyr Glu Glu
 1 5 10 15
 Thr Lys Gln Ser Asp Pro Ile Val Ala Asn Val Tyr Ile Glu Thr Gly
 20 25 30
 Trp Ala Val Asn Arg Leu Leu Asp Asn Asn Glu Leu Ser Pro Phe Asp
 35 40 45
 Asp Tyr Asp Arg Val Glu Lys Lys Ile Met Asn Glu Ile Asn Trp Lys
 50 55 60
 Lys Thr His Ile Lys Glu Cys
 65 70

<210> 5
 <211> 120
 <212> DNA
 <213> Staphylococcus aureus

<400> 5
 ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 60
 gtagaattac aaaaatacta ttacagcaa attgttgcta agaataaaga acgcatgtag 120

<210> 6
 <211> 39
 <212> PRT
 <213> Staphylococcus aureus

<400> 6
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr
 1 5 10 15
 Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val
 20 25 30
 Ala Lys Asn Lys Glu Arg Met
 35

<210> 7
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 cgcgatccc tatccttttt cattaataac attg 34

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
 ccggaattct tgcaataga tcaatcg 27

<210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 ggaagatctc tacatgcgtt ctttatcc 28

<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 ccggaattca tgataggttt gtgtcct 27

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccggaattcc caaaatacct aaatagtcc

29

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ccggaattcg cacataatga cctttca

27

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
cgcggatcca tgcctgatgg caattg

26

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
ccatcgatga tttcataagc gaaatata

28

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ccggaattcc ctgagccaat tggatatggc 29

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
cgcggtatccc taagggttcaa tgtaaccgcc 30

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
ccggaattca aggataactt cacaaatcag 30

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
cgcggtatccc tacttatcaa cactttcata ata 33

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
ccggaattca gagaaacact aattagctta 30

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

cgcgatccc tatctcaact catttgaatt aac

33

<210> 21

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

ccggaattcg gacaagaaac aattgagtc

29

<210> 22

<211> 581

<212> PRT

<213> Escherichia coli

<400> 22

Met	Ala	Gly	Arg	Ile	Pro	Arg	Val	Phe	Ile	Asn	Asp	Leu	Leu	Ala	Arg
1				5					10					15	

Thr	Asp	Ile	Val	Asp	Leu	Ile	Asp	Ala	Arg	Val	Lys	Leu	Lys	Lys	Gln
			20					25					30		

Gly	Lys	Asn	Phe	His	Ala	Cys	Cys	Pro	Phe	His	Asn	Glu	Lys	Thr	Pro
		35					40					45			

Ser	Phe	Thr	Val	Asn	Gly	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys
	50					55					60				

Gly	Ala	His	Gly	Asn	Ala	Ile	Asp	Phe	Leu	Met	Asn	Tyr	Asp	Lys	Leu
65					70					75					80

Glu	Phe	Val	Glu	Thr	Val	Glu	Glu	Leu	Ala	Ala	Met	His	Asn	Leu	Glu
				85					90					95	

Val	Pro	Phe	Glu	Ala	Gly	Ser	Gly	Pro	Ser	Gln	Ile	Glu	Arg	His	Gln
			100					105					110		

Arg	Gln	Thr	Leu	Tyr	Gln	Leu	Met	Asp	Gly	Leu	Asn	Thr	Phe	Tyr	Gln
		115				120						125			

Gln	Ser	Leu	Gln	Gln	Pro	Val	Ala	Thr	Ser	Ala	Arg	Gln	Tyr	Leu	Glu
	130					135					140				

Lys	Arg	Gly	Leu	Ser	His	Glu	Val	Ile	Ala	Arg	Phe	Ala	Ile	Gly	Phe
145					150					155					160

Ala	Pro	Pro	Gly	Trp	Asp	Asn	Val	Leu	Lys	Arg	Phe	Gly	Gly	Asn	Pro
				165					170					175	

Glu	Asn	Arg	Gln	Ser	Leu	Ile	Asp	Ala	Gly	Met	Leu	Val	Thr	Asn	Asp	
			180					185						190		
Gln	Gly	Arg	Ser	Tyr	Asp	Arg	Phe	Arg	Glu	Arg	Val	Met	Phe	Pro	Ile	
		195					200					205				
Arg	Asp	Lys	Arg	Gly	Arg	Val	Ile	Gly	Phe	Gly	Gly	Arg	Val	Leu	Gly	
	210					215					220					
Asn	Asp	Thr	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	Thr	Asp	Ile	Phe	His	
225					230					235					240	
Lys	Gly	Arg	Gln	Leu	Tyr	Gly	Leu	Tyr	Glu	Ala	Gln	Gln	Asp	Asn	Ala	
			245						250					255		
Glu	Pro	Asn	Arg	Leu	Leu	Val	Val	Glu	Gly	Tyr	Met	Asp	Val	Val	Ala	
		260						265					270			
Leu	Ala	Gln	Tyr	Gly	Ile	Asn	Tyr	Ala	Val	Ala	Ser	Leu	Gly	Thr	Ser	
		275					280					285				
Thr	Thr	Ala	Asp	His	Ile	Gln	Leu	Leu	Phe	Arg	Ala	Thr	Asn	Asn	Val	
	290					295					300					
Ile	Cys	Cys	Tyr	Asp	Gly	Asp	Arg	Ala	Gly	Arg	Asp	Ala	Ala	Trp	Arg	
305					310					315					320	
Ala	Leu	Glu	Thr	Ala	Leu	Pro	Tyr	Met	Thr	Asp	Gly	Arg	Gln	Leu	Arg	
			325						330					335		
Phe	Met	Phe	Leu	Pro	Asp	Gly	Glu	Asp	Pro	Asp	Thr	Leu	Val	Arg	Lys	
		340						345					350			
Glu	Gly	Lys	Glu	Ala	Phe	Glu	Ala	Arg	Met	Glu	Gln	Ala	Met	Pro	Leu	
		355					360					365				
Ser	Ala	Phe	Leu	Phe	Asn	Ser	Leu	Met	Pro	Gln	Val	Asp	Leu	Ser	Thr	
	370					375					380					
Pro	Asp	Gly	Arg	Ala	Arg	Leu	Ser	Thr	Leu	Ala	Leu	Pro	Leu	Ile	Ser	
385					390					395					400	
Gln	Val	Pro	Gly	Glu	Thr	Leu	Arg	Ile	Tyr	Leu	Arg	Gln	Glu	Leu	Gly	
			405						410					415		
Asn	Lys	Leu	Gly	Ile	Leu	Asp	Asp	Ser	Gln	Leu	Glu	Arg	Leu	Met	Pro	
		420						425					430			
Lys	Ala	Ala	Glu	Ser	Gly	Val	Ser	Arg	Pro	Val	Pro	Gln	Leu	Lys	Arg	
		435					440					445				
Thr	Thr	Met	Arg	Ile	Leu	Ile	Gly	Leu	Leu	Val	Gln	Asn	Pro	Glu	Leu	
	450					455					460					
Ala	Thr	Leu	Val	Pro	Pro	Leu	Glu	Asn	Leu	Asp	Glu	Asn	Lys	Leu	Pro	
465					470					475					480	

Gly Leu Gly Leu Phe Arg Glu Leu Val Asn Thr Cys Leu Ser Gln Pro
 485 490 495

Gly Leu Thr Thr Gly Gln Leu Leu Glu His Tyr Arg Gly Thr Asn Asn
 500 505 510

Ala Ala Thr Leu Glu Lys Leu Ser Met Trp Asp Asp Ile Ala Asp Lys
 515 520 525

Asn Ile Ala Glu Gln Thr Phe Thr Asp Ser Leu Asn His Met Phe Asp
 530 535 540

Ser Leu Leu Glu Leu Arg Gln Glu Glu Leu Ile Ala Arg Glu Arg Thr
 545 550 555 560

His Gly Leu Ser Asn Glu Glu Arg Leu Glu Leu Trp Thr Leu Asn Gln
 565 570 575

Glu Leu Ala Lys Lys
 580

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

ccgctcgagc tccaaattcc aaaacag

27

<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

cgggatccaa taagactcct ttttac

26

<210> 25

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

gcgcatctgt aaaaccacg

19

<210> 26
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
 gcacgaattc aagaagaatt g 21

<210> 27
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 27
 gatctcgtcg tgcattctgtt ggatccccgg aattccccggg 40

<210> 28
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 28
 tcgaccggg aattccggg atccaacaga tgcacgacga 40

<210> 29
 <211> 9
 <212> PRT
 <213> Staphylococcus aureus

<400> 29
 Tyr Tyr Leu Gln Gln Ile Val Ala Lys
 1 5

<210> 30
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 30
 Glu Leu Ser His Asp Ile Ser Leu Met Lys
 1 5 10

<210> 31
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 31
 Ile Asp Gln Ser Ile Ile Asn Glu Ile Lys
 1 5 10

<210> 32
 <211> 11
 <212> PRT
 <213> Staphylococcus aureus

<400> 32
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys
 1 5 10

<210> 33
 <211> 10
 <212> PRT
 <213> Staphylococcus aureus

<400> 33
 Asn Glu Glu Asn Phe Ser Tyr Tyr Asp Arg
 1 5 10

<210> 34
 <211> 12
 <212> PRT
 <213> Staphylococcus aureus

<400> 34
 Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln Lys
 1 5 10

<210> 35
 <211> 16
 <212> PRT
 <213> Staphylococcus aureus

<400> 35
 Lys Gly Tyr Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg
 1 5 10 15

<210> 36
 <211> 17
 <212> PRT
 <213> Staphylococcus aureus

<400> 36
 Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser Tyr Glu
 1 5 10 15

Arg

<210> 37

<211> 98

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Illustrative
zf-CHC2 comparison peptide

<400> 37

Ile	Pro	Glu	Glu	Ser	Ile	Asp	Glu	Leu	Lys	Asn	Arg	Ile	Asp	Ile	Val
1				5					10					15	

Asp	Val	Ile	Ser	Glu	Tyr	Val	Lys	Leu	Lys	Lys	Lys	Gly	Arg	Asn	Tyr
			20					25					30		

Lys	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe	Ser	Val
	35						40					45			

Ser	Pro	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Gly	Gly
	50					55					60				

Asp	Ala	Ile	Lys	Phe	Leu	Met	Lys	Tyr	Glu	Lys	Leu	Ser	Phe	Val	Glu
65					70					75					80

Ala	Val	Glu	Lys	Leu	Ala	Asp	Arg	Ala	Gly	Ile	Asp	Leu	Pro	Tyr	Glu
				85					90					95	

Lys Gly

<210> 38

<211> 151

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Illustrative
toprim comparison peptide

<400> 38

Lys	Val	Leu	Ile	Ile	Val	Glu	Gly	Pro	Ser	Asp	Ala	Lys	Ala	Leu	Ala
1				5					10					15	

Lys	Ala	Leu	Gly	Lys	Pro	Ser	Lys	Arg	Lys	Ile	Val	Tyr	Glu	Leu	Pro
		20						25					30		

Gly	Gly	Lys	Asp	Gly	Asn	Val	Val	Ala	Ser	Leu	Gly	His	Leu	Val	Asp
	35					40						45			

Leu	Pro	Thr	Pro	Glu	Gly	Tyr	Asp	Asp	Lys	Tyr	Lys	Trp	Leu	Trp	Leu
	50					55					60				

Pro Ile Val Asp Val Lys Lys Gly Phe Glu Pro Tyr Gln Ile Glu Phe
65 70 75 80

Asp Gln Leu Cys Lys Cys Ser Lys Lys Ile Asp Leu Lys Lys Glu Gln
85 90 95

Leu Lys Leu Leu Lys Lys Leu Ala Lys Lys Ala Asp Glu Val Ile Leu
100 105 110

Ala Thr Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp Lys Leu Leu
115 120 125

Glu Leu Leu Lys Pro Tyr Gly Pro Val Glu Leu Glu Asp Asp Lys Lys
130 135 140

Val Arg Arg Ile Phe Leu Pro
145 150

<210> 39
<211> 572
<212> PRT
<213> Staphylococcus aureus

<400> 39
Met Ile Gly Leu Cys Pro Phe His Asp Glu Lys Thr Pro Ser Phe Thr
1 5 10 15

Val Ser Glu Asp Lys Gln Ile Cys His Cys Phe Gly Cys Lys Lys Gly
20 25 30

Gly Asn Val Phe Gln Phe Thr Gln Glu Ile Lys Asp Ile Ser Phe Val
35 40 45

Glu Ala Val Lys Glu Leu Gly Asp Arg Val Asn Val Ala Val Asp Ile
50 55 60

Glu Ala Thr Gln Ser Asn Ser Asn Val Gln Ile Ala Ser Asp Asp Leu
65 70 75 80

Gln Met Ile Glu Met His Glu Leu Ile Gln Glu Phe Tyr Tyr Tyr Ala
85 90 95

Leu Thr Lys Thr Val Glu Gly Glu Gln Ala Leu Thr Tyr Leu Gln Glu
100 105 110

Arg Gly Phe Thr Asp Ala Leu Ile Lys Glu Arg Gly Ile Gly Phe Ala
115 120 125

Pro Asp Ser Ser His Phe Cys His Asp Phe Leu Gln Lys Lys Gly Tyr
130 135 140

Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg Asn Glu Glu
145 150 155 160

Asn Phe Ser Tyr Tyr Asp Arg Phe Arg Asn Arg Ile Met Phe Pro Leu
165 170 175

Lys Asn Ala Gln Gly Arg Ile Val Gly Tyr Ser Gly Arg Thr Tyr Thr
 180 185 190
 Gly Gln Glu Pro Lys Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln
 195 200 205
 Lys Arg Lys Leu Leu Tyr Asn Leu Asp Lys Ala Arg Lys Ser Ile Arg
 210 215 220
 Lys Leu Asp Glu Ile Val Leu Leu Glu Gly Phe Met Asp Val Ile Lys
 225 230 235 240
 Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr Gln
 245 250 255
 Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn Ile
 260 265 270
 Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu Lys
 275 280 285
 Thr Gly Gln His Leu Leu Gln Glu Gly Leu Asn Val Phe Val Ile Gln
 290 295 300
 Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly Asn
 305 310 315 320
 Asp Ala Phe Thr Thr Phe Val Lys Asn Asp Lys Lys Ser Phe Ala His
 325 330 335
 Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser
 340 345 350
 Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met Lys
 355 360 365
 Ser Ser Ile Leu Gln Gln Lys Ala Ile Asn Asp Val Ala Pro Phe Phe
 370 375 380
 Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln Ala
 385 390 395 400
 Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Asp Glu Tyr
 405 410 415
 Gly Gly Tyr Ile Glu Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn
 420 425 430
 Leu Ser Arg Arg Glu Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met
 435 440 445
 Arg Asp Lys Asp Thr Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp
 450 455 460
 Asn Phe Thr Asn Gln His Phe Lys Tyr Val Phe Glu Val Leu His Asp
 465 470 475 480

<400> 40																
Met	Gly	His	Arg	Ile	Pro	Glu	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Arg	Gly	
1				5					10					15		
Val	Asp	Ile	Val	Asp	Val	Ile	Gly	Glu	Tyr	Val	Gln	Leu	Lys	Arg	Gln	
			20					25					30			
Gly	Arg	Asn	Tyr	Phe	Gly	Leu	Cys	Pro	Phe	His	Gly	Glu	Lys	Thr	Pro	
		35					40					45				
Ser	Phe	Ser	Val	Ser	Pro	Glu	Lys	Gln	Ile	Phe	His	Cys	Phe	Gly	Cys	
	50					55					60					
Gly	Ala	Gly	Gly	Asn	Ala	Phe	Thr	Phe	Leu	Met	Asp	Ile	Glu	Gly	Ile	
65					70					75					80	
Pro	Phe	Val	Glu	Ala	Ala	Lys	Arg	Leu	Ala	Ala	Lys	Ala	Gly	Val	Asp	
				85					90					95		
Leu	Ser	Val	Tyr	Glu	Leu	Asp	Val	Arg	Gly	Arg	Asp	Asp	Gly	Gln	Thr	
			100					105					110			
Asp	Glu	Ala	Lys	Ala	Met	Thr	Glu	Ala	His	Ala	Leu	Leu	Lys	Arg	Phe	
		115					120					125				
Tyr	His	His	Leu	Leu	Val	His	Thr	Lys	Glu	Gly	Gln	Ala	Ala	Leu	Asp	
	130					135					140					
Tyr	Leu	Gln	Ala	Arg	Gly	Trp	Thr	Lys	Glu	Thr	Ile	Asp	Arg	Phe	Glu	
145					150					155					160	
Ile	Gly	Tyr	Ala	Pro	Asp	Ala	Pro	Asp	Ala	Ala	Ala	Lys	Leu	Leu	Glu	
				165					170					175		

Ser His Ser Phe Ser Leu Pro Val Met Glu Lys Ala Gly Leu Leu Thr
 180 185 190
 Lys Lys Glu Asp Gly Arg Tyr Val Gly Arg Phe Arg Asn Arg Ile Met
 195 200 205
 Phe Pro Ile His Asp His Arg Gly Glu Thr Val Gly Phe Ser Gly Arg
 210 215 220
 Leu Leu Gly Glu Gly His Pro Lys Tyr Val Asn Ser Pro Glu Thr Pro
 225 230 235 240
 Val Phe Arg Lys Gly Ala Ile Leu Tyr His Phe His Ala Ala Arg Val
 245 250 255
 Pro Ile Arg Lys Arg Gln Glu Ala Leu Leu Val Glu Gly Phe Ala Asp
 260 265 270
 Val Ile Ser Ala Ala Gln Ala Gly Ile Asp Tyr Ala Ile Ala Thr Met
 275 280 285
 Gly Thr Ser Leu Thr Glu Glu Gln Ala Arg Ile Leu Arg Pro Cys Asp
 290 295 300
 Thr Ile Thr Ile Cys Tyr Asp Gly Asp Arg Ala Gly Ile Glu Ala Ala
 305 310 315 320
 Trp Ala Ala Ala Glu Gln Leu Ser Ala Leu Gly Cys Arg Val Lys Val
 325 330 335
 Ala Ser Leu Pro Asn Gly Leu Asp Pro Asp Glu Tyr Ile Arg Val Tyr
 340 345 350
 Gly Gly Glu Arg Phe Ala Gly Glu Ala Gly Cys Arg Arg Pro Leu Val
 355 360 365
 Ala Phe Lys Met Ala Tyr Leu Arg Arg Gly Lys Asn Leu Gln His Glu
 370 375 380
 Gly Glu Arg Leu Arg Tyr Ile Asp Glu Ala Leu Arg Glu Ile Gly Lys
 385 390 395 400
 Leu Ser Ser Pro Val Glu Gln Asp Tyr Tyr Leu Arg Gln Leu Ala Glu
 405 410 415
 Glu Phe Ser Leu Ser Leu Ser Ala Leu His Glu Gln Leu Ser Arg Ser
 420 425 430
 Gln Arg Glu Arg Thr Lys Pro Arg Glu Ala Pro Asp Gly Glu Thr Ala
 435 440 445
 Arg Pro Met Leu Ala Lys Lys Leu Leu Pro Ala Phe Gln Asn Ala Glu
 450 455 460
 Arg Leu Leu Leu Ala His Met Met Arg Ser Arg Asp Val Ala Leu Val
 465 470 475 480

Val Gln Glu Arg Ile Gly Gly Arg Phe Asn Ile Glu Glu His Arg Ala
 485 490 495

Leu Ala Ala Tyr Ile Tyr Ala Phe Tyr Glu Glu Gly His Glu Ala Asp
 500 505 510

Pro Gly Ala Leu Ile Ser Arg Ile Pro Gly Glu Leu Gln Pro Leu Ala
 515 520 525

Ser Asp Val Ser Leu Leu Leu Ile Ala Asp Asp Val Ser Glu Gln Glu
 530 535 540

Leu Glu Asp Tyr Ile Arg His Val Leu Asn Arg Pro Lys Trp Leu Met
 545 550 555 560

Leu Lys Val Lys Glu Gln Glu Lys Thr Glu Ala Glu Arg Arg Lys Asp
 565 570 575

Phe Leu Thr Ala Ala Arg Ile Ala Lys Glu Met Ile Glu Met Lys Lys
 580 585 590

Met Leu Ser Ser Ser
 595

<210> 41

<211> 603

<212> PRT

<213> *Bacillus subtilis*

<400> 41

Met Gly Asn Arg Ile Pro Asp Glu Ile Val Asp Gln Val Gln Lys Ser
 1 5 10 15

Ala Asp Ile Val Glu Val Ile Gly Asp Tyr Val Gln Leu Lys Lys Gln
 20 25 30

Gly Arg Asn Tyr Phe Gly Leu Cys Pro Phe His Gly Glu Ser Thr Pro
 35 40 45

Ser Phe Ser Val Ser Pro Asp Lys Gln Ile Phe His Cys Phe Gly Cys
 50 55 60

Gly Ala Gly Gly Asn Val Phe Ser Phe Leu Arg Gln Met Glu Gly Tyr
 65 70 75 80

Ser Phe Ala Glu Ser Val Ser His Leu Ala Asp Lys Tyr Gln Ile Asp
 85 90 95

Phe Pro Asp Asp Ile Thr Val His Ser Gly Ala Arg Pro Glu Ser Ser
 100 105 110

Gly Glu Gln Lys Met Ala Glu Ala His Glu Leu Leu Lys Lys Phe Tyr
 115 120 125

His His Leu Leu Ile Asn Thr Lys Glu Gly Gln Glu Ala Leu Asp Tyr
 130 135 140

Leu Leu Ser Arg Gly Phe Thr Lys Glu Leu Ile Asn Glu Phe Gln Ile
 145 150 155 160
 Gly Tyr Ala Leu Asp Ser Trp Asp Phe Ile Thr Lys Phe Leu Val Lys
 165 170 175
 Arg Gly Phe Ser Glu Ala Gln Met Glu Lys Ala Gly Leu Leu Ile Arg
 180 185 190
 Arg Glu Asp Gly Ser Gly Tyr Phe Asp Arg Phe Arg Asn Arg Val Met
 195 200 205
 Phe Pro Ile His Asp His His Gly Ala Val Val Ala Phe Ser Gly Arg
 210 215 220
 Ala Leu Gly Ser Gln Gln Pro Lys Tyr Met Asn Ser Pro Glu Thr Pro
 225 230 235 240
 Leu Phe His Lys Ser Lys Leu Leu Tyr Asn Phe Tyr Lys Ala Arg Leu
 245 250 255
 His Ile Arg Lys Gln Glu Arg Ala Val Leu Phe Glu Gly Phe Ala Asp
 260 265 270
 Val Tyr Thr Ala Val Ser Ser Asp Val Lys Glu Ser Ile Ala Thr Met
 275 280 285
 Gly Thr Ser Leu Thr Asp Asp His Val Lys Ile Leu Arg Arg Asn Val
 290 295 300
 Glu Glu Ile Ile Leu Cys Tyr Asp Ser Asp Lys Ala Gly Tyr Glu Ala
 305 310 315 320
 Thr Leu Lys Ala Ser Glu Leu Leu Gln Lys Lys Gly Cys Lys Val Arg
 325 330 335
 Val Ala Met Ile Pro Asp Gly Leu Asp Pro Asp Asp Tyr Ile Lys Lys
 340 345 350
 Phe Gly Gly Glu Lys Phe Lys Asn Asp Ile Ile Asp Ala Ser Val Thr
 355 360 365
 Val Met Ala Phe Lys Met Gln Tyr Phe Arg Lys Gly Lys Asn Leu Ser
 370 375 380
 Asp Glu Gly Asp Arg Leu Ala Tyr Ile Lys Asp Val Leu Lys Glu Ile
 385 390 395 400
 Ser Thr Leu Ser Gly Ser Leu Glu Gln Glu Val Tyr Val Lys Gln Leu
 405 410 415
 Ala Ser Glu Phe Ser Leu Ser Gln Glu Ser Leu Thr Glu Gln Leu Ser
 420 425 430
 Val Phe Ser Lys Gln Asn Lys Pro Ala Asp Asn Ser Gly Glu Thr Lys
 435 440 445

Thr Arg Arg Ala His Leu Thr Thr Lys Ala Arg Gln Lys Arg Leu Arg
 450 455 460
 Pro Ala Tyr Glu Asn Ala Glu Arg Leu Leu Leu Ala His Met Leu Arg
 465 470 475 480
 Asp Arg Ser Val Ile Lys Lys Val Ile Asp Arg Val Gly Phe Gln Phe
 485 490 495
 Asn Ile Asp Glu His Arg Ala Leu Ala Ala Tyr Leu Tyr Ala Phe Tyr
 500 505 510
 Glu Glu Gly Ala Glu Leu Thr Pro Gln His Leu Met Ala Arg Val Thr
 515 520 525
 Asp Asp His Ile Ser Gln Leu Leu Ser Asp Ile Leu Met Leu Gln Val
 530 535 540
 Asn Gln Glu Leu Ser Glu Ala Glu Leu Ser Asp Tyr Val Lys Lys Val
 545 550 555 560
 Leu Asn Gln Arg Asn Trp Ser Met Ile Lys Glu Lys Glu Ala Glu Arg
 565 570 575
 Ala Glu Ala Glu Arg Gln Lys Asp Phe Leu Arg Ala Ala Ser Leu Ala
 580 585 590
 Gln Glu Ile Val Thr Leu Asn Arg Ser Leu Lys
 595 600

A^v
 cont.